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175928

From: Mertz, Prema
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Please search SEQ ID NO:6 with protein databases.

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Searcher: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
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OM protein - protein search, using sw model

Run on: January 10, 2006, 22:51:05 ; Search time 160 Seconds
(without alignments)
326.307 Million cell updates/sec

Title: US-10-760-557-6

Perfect score: 416
Sequence: 1 TKTSSSRGRPHSECCPTT.....VCTNPSDKMVDYIKDKKEN 74

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	416	100.0	93	1 CCL14_HUMAN	Q16627 homo sapien
2	230	55.3	93	2 Q6DUR4_PIG	Q6dura sus scrofa
3	226	54.3	92	2 Q711P4_PIG	Q711p4 sus scrofa
4	221	53.1	92	2 Q8HYQ3_MACMU	Q8hyq3 macaca mula
5	220	52.9	92	2 Q8HYQ2_MACMU	Q8hyq2 macaca mula
6	219	52.6	92	1 CCL13_HUMAN	P10147 h small ind
7	218	52.4	92	1 CCL14_MOUSE	P14097 mus musculu
8	218	52.4	92	2 Q8NHW4_HUMAN	Q8nhw4 homo sapien
9	218	52.4	92	2 Q5QNV9_MOUSE	Q5qnv9 mus musculu
10	218	52.4	93	1 CCL3L_HUMAN	P16619 homo sapien
11	218	52.4	93	2 Q53YA5_HUMAN	Q53ya5 homo sapien
12	216	51.9	92	1 CCL14_RABIT	P46632 oryctolagus
13	214	51.4	90	2 Q4VSK4_CANAPL	Q4vsk4 anas platyr
14	214	51.4	92	2 Q68A20_CANPA	Q68a20 canis famli
15	213	51.2	92	1 CCL3_PANTR	Q51120 pan troglod
16	213	51.2	92	1 CCL4_RAT	P50230 rattus norv
17	213	51.2	92	2 Q6NSB0_HUMAN	Q6nsb0 homo sapien
18	213	51.2	92	2 Q91ZL0_SIGHI	Q91zl0 sigmodon hi
19	212	51.0	92	1 CCL4_HUMAN	P13336 h small ind
20	212	51.0	92	2 Q6FGI8_HUMAN	Q6fgi8 homo sapien
21	211	50.7	93	1 CCL3_BOVIN	Q89ga6 bos taurus
22	209	50.2	93	2 Q8HYN4_MACMU	Q8hyn4 macaca mula
23	209	50.2	90	2 Q9PWA6_CHICK	Q9pwa6 gallus faml
24	209	50.2	92	1 CCL3_CANPA	Q68a92 canis famli
25	207	49.8	80	2 Q14745_HUMAN	Q14745 homo sapien
26	206	49.5	90	1 CCL4_CHICK	Q90826 gallus gall
27	201.5	48.4	89	2 Q91E00_CHICK	Q91e00 gallus gall
28	201.5	48.4	89	2 Q4KX30_CHICK	Q4kx30 gallus gall
29	201	48.3	89	1 CCL18_HUMAN	P55774 h small ind
30	201	48.3	89	2 Q53Y71_HUMAN	Q53y71 homo sapien
31	200.5	48.2	92	1 CCL13_MOUSE	P10855 mus musculu

32	200.5	48.2	92	2 Q5QNM0_MOUSE	Q5qnm0 mus musculu
33	195	46.9	85	2 Q80XG5_PERMA	Q80xg5 peromyscus
34	191.5	46.0	92	1 CCL3_RAT	P50223 rattus norv
35	187.5	45.1	87	2 Q5QEW7_HUMAN	Q5qew7 homo sapien
36	184	44.2	88	1 CCL18_MACMU	Q8hyr8 macaca mula
37	183.5	44.1	92	2 Q91Z65_SIGHI	Q91z65 sigmodon hi
38	176	42.3	49	2 Q8HYN3_MACMU	Q8hyn3 macaca mula
39	176	42.3	120	1 CCL123_HUMAN	P55773 homo sapien
40	176	42.3	120	2 Q521D4_HUMAN	Q521d4 homo sapien
41	174	41.8	101	2 Q64IC2_ONCMW	Q64ic2 oncorhynch
42	172	41.3	91	2 CCL5_HORSE	Q6nk0 equus caball
43	172	41.3	91	1 CCL5_HUMAN	P13501 homo sapien
44	171.5	41.2	98	2 Q5PY11_MESAU	Q5py11 mesocricetu
45	170.5	41.0	119	2 Q8K477_RAT	Q8k477 rattus norv

ALIGNMENTS

RESULT 1

CCL14_HUMAN STANDARD, PRT; 93 AA.
ID CCL14_HUMAN Q16627; Q13954;
AC Q16627; Q13954; (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Small inducible cytokine A14 precursor (CCL14) (Chemokine CC-1/CC-3) (HCC-1/HCC-3) (HCC-1(1-74)) (NCC-2) [Contains: HCC-1(3-74); HCC-1(4-74); HCC-1(9-74)].
GN Name=CCL14; Synonyms=NCC2, SCYA14;
DS Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 20-93.
RC TISSUE=Bone marrow;
RX MEDLINE=96136773; PubMed=8551235; DOI=10.1084/jem.183.1.295; Schultz-Knappe P., Maegert H.-U., Dewald B., Meyer M., Cetin Y., Rubbles M., Tomeczkowski J., Kirchhoff K., Raida M., Ademann K., Kist A., Reinecke M., Sillard R., Paridgol A., Uguccloni M., Baggiolini M., Forssmann W.-G.; "HCC-1, a novel chemokine from human plasma."; J. Exp. Med. 183:295-299(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=98263352; PubMed=9600961; DOI=10.1073/pnas.95.11.6308; Paridgol A., Forssmann U., Zucht H.-D., Loetscher P., Schulz-Knappe P., Baggiolini M., Forssmann W.-G., Maegert H.-U.; "HCC-2, a human chemokine: gene structure, expression pattern, and biological activity."; Proc. Natl. Acad. Sci. U.S.A. 95:6308-6313(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99228475; PubMed=10213461; DOI=10.1089/107999099314153; Nomyama H., Fukuda S., Ito M., Tanase S., Miura K., Yoshie O.; "Organization of the chemokine gene cluster on human chromosome 17q11.2 containing the genes for CC chemokine MIP-1, HCC-2, IEC, and RANTES."; J. Interferon Cytokine Res. 19:227-234(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM HCC-1).
RC TISSUE=pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altchul S.F., Zeebrow B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S, Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boask S.A., McGowan P.J., McKernan K.J., Malek J.A., Ganatrane P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywicki M.T., Skalski U., Smalhus D.E.,
 RA Schermer A., Schin J.E., Jones S.J.M., Marra N.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL
 RN [5]
 RN PROTEIN SEQUENCE OF 20-32, IDENTIFICATION OF HCC-1(3-74) AND
 RP HCC-1(4-74), MASS SPECTROMETRY, AND CARBOHYDRATE-LINKAGE SITE SER-26.
 RP Published:1097815; DOI=10.1021/b1992488q;
 RX Richter R., Schulz-Knappe P., John H., Forssmann W.-G.,
 RA "Posttranslational processing of the human chemokine HCC-1-".
 RL Biochemistry 39:10799-10805 (2000).
 [6]
 RN PROTEIN SEQUENCE OF 20-48, IDENTIFICATION OF HCC-1(9-74), MASS
 RP SPECTROMETRY, AND FUNCTION.
 RP Published:1085751; DOI=10.1084/jem.192.10.1501;
 RX DeFeux M., Staendker L., Vakil J., Muench U., Forssmann U.,
 RA Adtmann K., Poehlmann S., Vassart G., Kirchhoff P., Parmentier M.,
 RA Forssmann W.-G.,
 RA "Natural proteolytic processing of hemofiltrate CC chemokine 1
 RT generates a potent CC chemokine receptor (CCR1) and CCR5 agonist with
 RT anti-HIV properties.";
 RL J. Exp. Med. 192:1051-1058 (2000).
 CC -1- FUNCTION: Has weak activities on human monocytes and acts via
 CC receptors that also recognize MIP-1 alpha. It induced
 CC intracellular Ca(2+) changes and enzyme release, but no
 CC chemotaxis, at concentrations of 100-1,000 nM, and was inactive on
 CC T lymphocytes, neutrophils, and eosinophil leukocytes. Enhances
 CC the proliferation of CD34 myeloid progenitor cells. The processed
 CC form HCC-1(9-74) is a chemotactic factor that attracts monocytes
 CC eosinophils, and T cells and is a ligand for CCR1, CCR3 and CCR5.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=HCC-1;
 CC IsoId=Q16627-1; Sequence=Displayed;
 CC Name=HCC-3;
 CC IsoId=Q16627-2; Sequence=VSP_001060;
 CC -1- TISSUE SPECIFICITY: Expressed constitutively in several normal
 CC tissues: spleen, liver, skeletal and heart muscle, gut, and bone
 CC marrow, present at high concentrations (1-80 nM) in plasma.
 CC -1- PTM: The N-terminal processed forms HCC-1(3-74), HCC-1(4-74) and
 CC HCC-1(9-74) are produced in small amounts by proteolytic cleavage
 CC after secretion in blood.
 CC -1- PTM: HCC-1(1-74), but not HCC-1(3-74) and HCC-1(4-74), is
 CC partially O-glycosylated; the O-linked glycan consists of one gal-
 CC NAc6 disaccharide, further modified by two N-acetylneuraminic
 CC acids.
 CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL, Z49370, CA869264.1, -, mRNA.
 DR EMBL, Z70592, CA943507.1, -, mRNA.
 DR EMBL, Z70593, CA943509.1, -, mRNA.
 DR EMBL, Z49269, CA869263.1, -, Genomic_DNA.
 DR EMBL, AF088219, AAC65382.1, -, Genomic_DNA.
 DR EMBL, AF088219, AAC23982.1, -, Genomic_DNA.
 DR EMBL, BC048289, AAH38289.1, -, mRNA.
 DR EMBL, BC045165, AAH45165.1, -, mRNA.
 DR HSSP, P13236, IHDM.

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DR HGNC; HGNC:10612; CCL14.
DR MIM; 601392; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004871; P:signal transducer activity; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR001811; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Alternative splicing; Cytokine; Direct protein sequencing;
KW Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 20
FT CHAIN 22
FT CHAIN 23
FT CHAIN 28
FT CHAIN 26
FT CHAIN 35
FT DISULFID 36
FT DISULFID 37
FT VARSPPLIC 27
FT FT
FT FT
SQ SEQUENCE 93 AA; 10678 MW; 10678 MW; 10678 MW;
Query March 100.0%; Score 416; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 5,7e-19;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TKTSSSRGPHYSECCFTYTYTKIPRQIMDYETNSQSKPGIVITRKGHSVCTNPS 60
DB 20 TKTSSSRGPHYSECCFTYTYTKIPRQIMDYETNSQSKPGIVITRKGHSVCTNPS 79
OY 61 DKWVDYIKDKMEN 74
DB 80 DKWVDYIKDKMEN 93
RESULT 2
06DURK4_PIG PRELIMINARY; PRT; 93 AA.
AC 06DURK4_PIG
DT 25-OCT-2004 (Tremblere1.28, Created)
DT 25-OCT-2004 (Tremblere1.28, Last sequence update)
DT 25-OCT-2004 (Tremblere1.28, Last annotation update)
DE Macrophage inflammatory protein 1 alpha.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_TaxID=9623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stirling C.M.A.; Takamatsu H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY643423; AAT65077.1; -. mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 93 AA; 10117 MW; 08BD26CAE928414C CRC64;
Query Match 55.3%; Score 230; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5,7e-19;
Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;
OY 5 SSRGPHYSECCFTYTYTKIPRQIMDYETNSQSKPGIVITRKGHSVCTNPSDKW 64

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Db 23 SAPLADPTACCFSTYTSRQLPRKRVADYFETNSQCSKPGVIFQTKRGREVCANPEDAMV 82
QY 65 QDYIKDMKEN 74
Db 83 QEYISDLEIN 92

RESULT 3
Q711P4_PIG PRELIMINARY; PRT; 92 AA.
ID Q711P4_PIG PRELIMINARY; PRT; 92 AA.
AC Q711P4_PIG PRELIMINARY; PRT; 92 AA.
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE Putative MIP-1beta protein.
GN Name=MIP-1beta;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub. NCBI_TaxID=9823;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ezquerria A.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311717; CAC84398.1; mRNA.
DR HSSP; P10147; 1B50.
DR SMR; Q711P4; 24-92.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemokine response; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR InterPro; IPR000827; CC:chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10207 MW; ABIEQAESEAGF70E5 CRC64;

Query Match 54.3%; Score 226; DB 2; Length 92;
Best Local Similarity 54.3%; Pred. No. 1.6e-17;
Matches 38; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY 5 SSSRGPYHPSCEFFTYTYKIPRORIMDYETNSQCSKPGVIFITRGHGVCTNPBDDKV 64
Db 23 SAPMGSDPTSCFFTYTAKLRNPFVTDYETNSLCSQPAVVFQTKRGQVCANPSDDMV 82
QY 65 QDYIKDMKEN 74
Db 83 QEYMDLEIN 92

RESULT 4
Q8HYO3_MACMU PRELIMINARY; PRT; 92 AA.
ID Q8HYO3_MACMU PRELIMINARY; PRT; 92 AA.
AC Q8HYO3_MACMU PRELIMINARY; PRT; 92 AA.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Chemokine CCL4/MIP-1ADPHA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baas S.; Schaefer T.M.; Ghosh M.; Fuller C.L.; Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT and CX3C families of chemokines."
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RL Cytokine 18:140-148(2002).
DR EMBL; AF449266; AAN76070.1; mRNA.
DR HSSP; P10147; 1B50.
DR SMR; Q8HYO3; 24-92.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemokine response; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR InterPro; IPR000827; CC:chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10120 MW; 021CAA371143D12A CRC64;

Query Match 53.1%; Score 221; DB 2; Length 92;
Best Local Similarity 56.7%; Pred. No. 5.8e-17;
Matches 34; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 13 PSECCFTYTYKIPRORIMDYETNSQCSKPGVIFITRGHGVCTNPBDDKVQDYIKDMK 72
Db 30 PTCSCFSTYTSRQIFQNFVADYFETNSQCSKPGVIFITRGHGVQVCANPSKQVQKYSLE 89

RESULT 5
Q8HYO2_MACMU PRELIMINARY; PRT; 92 AA.
ID Q8HYO2_MACMU PRELIMINARY; PRT; 92 AA.
AC Q8HYO2_MACMU PRELIMINARY; PRT; 92 AA.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Chemokine CCL4/MIP-1BETA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baas S.; Schaefer T.M.; Ghosh M.; Fuller C.L.; Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT and CX3C families of chemokines";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449267; AAN76071.1; mRNA.
DR HSSP; P13236; 1HDM.
DR SMR; Q8HYO2; 24-92.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemokine response; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR InterPro; IPR000827; CC:chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10103 MW; 80B2C2071565F809 CRC64;

Query Match 52.9%; Score 220; DB 2; Length 92;
Best Local Similarity 51.4%; Pred. No. 7.5e-17;
Matches 36; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 5 SSSRGPYHPSCEFFTYTYKIPRORIMDYETNSQCSKPGVIFITRGHGVCTNPBDDKV 64
Db 23 SAPMGSDPTSCFFTYTAKLRNPFVTDYETNSLCSQPAVVFQTKRGQVCANPSDDMV 82
QY 65 QDYIKDMKEN 74
Db 83 QEYMDLEIN 92

RESULT 6
```

CCL3_HUMAN STANDARD; PRT; 92 AA.
ID CCL3_HUMAN
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
protein 1-alpha) (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha
protein) (G0/G1 switch regulatory protein 19-1) (G0S19-1 protein)
DE (SIS-beta) (PAT 464.1) [Contains: MIP-1-alpha(4-69) (LD78-alpha(4-
69))].
GN Name=CCL3; Synonyms=G0S19-1, MIP1A, SCVA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=6223879; PubMed=3086300;
RX Obaru K., Fukuda M., Maeda S., Shimada K.;
RT "A cDNA clone used to study mRNA inducible in human tonsillar
lymphocytes by a tumor promoter.";
RL J. Biochem. 99:885-894(1986).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=89140347; PubMed=2521882;
RX Zipfel F.F., Balke U., Irving S.G., Kelly K., Siebenlist U.;
RT "Mitogen activation of human T cells induces two closely related
genes which share structural similarities with a new family of
secreted factors.";
RL J. Immunol. 142:1582-1590(1989).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=91103879; PubMed=2271120;
RX Blum S., Forsdyke R.E., Forsdyke D.R.;
RT "Three human homologs of a murine gene encoding an inhibitor of stem
cell proliferation.";
RL DNA Cell Biol. 9:589-602(1990).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=90287155; PubMed=1694014;
RX Nakao M., Nomiyama H., Shimada K.;
RT "Structures of human genes coding for cytokine LD78 and their
expression.";
RL Mol. Cell. Biol. 10:3646-3658(1990).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Blood;
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Spletton M., Soares T.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein H.J., Uebachs T.B., Toshiyuki S., Canninci P., Prange C.J.,
RA Raba S.S., Loughell N.A., Peters G.J., Patterson R.D., Mullaly S.J.,
RA Bobak S.A., McKernan F.J., McKernan K.J., Malick J., Galy L., Hilyk S.W.,
RA Richards D.K., Morley K.C., Hale S., Garcia A.W., Lu X., Gibbs R.A.,
RA Villalón D.K., Wozny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE OF 23-92.
RX Jang J.S., Kim B.E.,

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN PROTEIN SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.
RX MEDLINE=96127782; PubMed=8541527;
RA Hunter M.G., Bowden L., Brotherton D., Craig S., Cribbes S.,
RA Chaplewski L.G., Dexter T.M., Drummond A.H., Geating A.H.,
RA Heyworth C.M., Lord B.I., Mccourt M., Varley P.G., Wood L.M.,
RA Edwards R.M., Lewis P.J.;
RT "BB-10010: an active variant of human macrophage inflammatory protein-
1 alpha with improved pharmaceutical properties.";
RL Blood 86:4400-4408(1995).
RN PROTEIN SEQUENCE OF 27-40 AND 71-83, AND FUNCTION.
RX MEDLINE=96106406; PubMed=8525373;
RA Cocchi F., Devico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
RA Lusso P.;
RT "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major
RT HIV-suppressive factors produced by CD8+ T cells.";
RL Science 270:1811-1815(1995).
RN PROTEIN SEQUENCE OF 27-51, AND IDENTIFICATION OF LD78-ALPHA(4-69).
RX MEDLINE=95251928; PubMed=7537510;
RA Bertini R., Iuini M., Sozzani S., Botzaz B., Ruggiero P.,
RA Boraschi D., Saggiaro D., Chicco-Blanchi L., Probst P., Van Damme J.,
RA Mantovani A.;
RT "Identification of MIP-1 alpha/LD78 as a monocyte chemottractant
RT released by the HIV-1-transformed cell line MT4.";
RL AIDS Res. Hum. Retroviruses 11:155-160(1995).
RN SHUNT, AND INTERACTION WITH MIP-1-BETA(3-69).
RX MEDLINE=2213107; PubMed=12070155; DOI=10.1074/jbc.M203077200;
RA Guan B., Wang J., Rodriguez G., Norcross M.A.;
RT "Natural truncation of the chemokine MIP-1beta/CCL4 affects receptor
RT specificity but not anti-HIV-1 activity.";
RL J. Biol. Chem. 277:32348-32352(2002).
RN REVIEW.
RX MEDLINE=22288990; PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;
RA Menten P., Whyte A., Van Damme J.;
RT "Macrophage inflammatory protein-1.";
RL Cytokine Growth Factor Rev. 13:455-481(2002).
RN STRUCTURE BY NMR OF 24-92, AND MUTAGENESIS OF ASP-49 AND GLU-89.
RX MEDLINE=99278370; PubMed=10347159; DOI=10.1074/jbc.274.23.16077;
RA Czaplinski L.G., McKeating J., Craven C.J., Higgins L.D., Appay V.,
RA Brown A., Dudgeon T., Howard L.A., Meyers T., Owen J., Palan S.R.,
RA Tan P., Wilson G., Woods N.R., Heyworth C.M., Lord B.I.,
RA Brotherton D., Christison R., Craig S., Cribbes S., Edwards R.M.,
RA Evans S.J., Gilbert R., Morgan P., Elliot Randle B., Schofield N.,
RA Varley P.G., Fisher J., Jonathan P., Walto J.P., Hunter M.G.;
RT "Identification of amino acid residues critical for aggregation of
RT human CC chemokines macrophage inflammatory protein (MIP)-1alpha, MIP-
RT 1beta, and RANTES. Characterization of active disassembled chemokine
RT variants.";
RL J. Biol. Chem. 274:16077-16084(1999).
RN FUNCTION. Monokine with inflammatory and chemokine properties.
CC Binds to CCR1, CCR4 and CCR5. One of the major HIV-suppressive
CC factors produced by CD8+ T cells. Recombinant MIP-1-alpha induces
CC a dose-dependent inhibition of different strains of HIV-1, HIV-2,
CC and simian immunodeficiency virus (SIV).
CC -1 SUBUNIT: Self-associates. Also heterodimer of MIP-1-alpha(4-69)
CC and MIP-1-beta(3-69).
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 INDUCTION: by IFN or PHA (IFN = 12-O-tetradecanoyl phorbol-13
CC acetate (tumor promoter); PHA = phytohemagglutinin (T-cell
CC mitogen)).
CC -1 PTM: N-terminal processed form LD78-alpha(4-69) is produced by
CC proteolytic cleavage after secretion from HIV-1-transformed T-
CC cells.
CC -1 SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

RESULT 7		
CCI4_MOUSE		
ID	CCI4_MOUSE	
AC	P14057;	
	STANDARD;	PRT;
		92 AA.

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
 protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2).
 GN Name=Ccl4; Synonyms=Mip1b, Scy4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89067830; PubMed=3058856; DOI=10.1084/jem.168.6.2251;
 RA Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G.,
 RA Wolpe S.D., Masiarz F., Colt D., Cerami A.;
 RT "Resolution of the two components of macrophage inflammatory protein
 RT derived inflammatory agents, growth factors, and indicators of various
 RT activated processes.";
 RL J. Immunol. 142:679-687 (1989).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DMB/20; TISSUE=Liver;
 RA Dabersies P., Lepretre F., Baillet B., Grove M., Pragnell I.,
 RA Plumb M.A.;
 RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn B.P.;
 RT "Sequence polymorphisms in the chemokines Sca1 (TCA-3), Scy2
 RT (monocyte chemoattractant protein (MCP)-1), and Sca12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2267-2266 (1999).
 CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the Interleukin beta (chemokine CC) family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL, M23503; AAA40148.1; -; mRNA.
 CC EMBL, M35590; AAA39708.1; -; mRNA.
 CC EMBL, X62502; CAA4364.1; -; genomic DNA.
 CC EMBL, AF128218; AAF22559.1; -; mRNA.
 CC EMBL, AF128219; AAF22560.1; -; mRNA.
 CC PIR, C30552; C30552.
 CC HSSP, P13236; IHDM.
 CC SRR, P14097; 24-92.
 CC Ensemble1; ENSMUSG00000018930; Mus musculus.
 CC MGI, MGI:98261; Ccl4.
 CC GO, GO:0005615; C:extracellular space; TAS.
 CC GO, GO:0005515; F:protein binding; IPI.
 CC InterPro, IPR000827; CC chemokine sml.
 CC InterPro, IPR001811; Chemokine Il8.
 CC InterPro, IPR008105; Lymphotactin.
 CC Pfam, PF00048; Il8; 1.

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91103879; PubMed=2277120;
 RA Blum S., Forsdyke R.E., Forsdyke D.R.;
 RT "Three human homologs of a murine gene encoding an inhibitor of stem
 cell proliferation";
 RL DNA Cell Biol. 9:589-602 (1990).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90287155; PubMed=1694014;
 RA Nakao M., Nomiyama H., Shimada K.;
 RT "Structure of human genes coding for cytokine LD78 and their
 expression";
 RL Mol. Cell. Biol. 10:3646-3658 (1990).
 [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=pancreas, spleen, and spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stedelson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueda T.B., Tashyuk S., Carninci P., Prange C.,
 Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gutarra P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,
 Roderick T., Schin J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]
 RP PROTEIN SEQUENCE OF 24-38.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 verified cleavage sites";
 RL Protein Sci. 13:2819-2824 (2004).
 [6]
 RP IDENTIFICATION OF LD78-BETA(3-70) AND LD78-BETA(5-70), N-TERMINAL
 PROCESSING AND FUNCTION.
 RX MEDLINE=20417739; PubMed=10961862;
 RA Proost P., Menten P., Struyf S., Schutysse E., De Weester I.,
 Van Damme J.;
 RT "Cleavage by CD26/dipeptidyl peptidase IV converts the chemokine
 LD78beta into a most efficient monocyte attractant and CCR1 agonist";
 RL Blood 96:1674-1680 (2000).
 -I- FUNCTION: Chemotactic for monocytes. Is a ligand for CCR5.
 Recombinant small inducible cytokine B10 induces a dose-dependent
 inhibition of macrophage tropic HIV-1 strains. The processed form
 LD78-beta(3-70) shows a 20-fold to 30-fold higher chemotactic
 activity and is also a ligand for CCR1.
 -I- SUBCELLULAR LOCATION: Secreted.
 -I- PTM: The N-terminal processed forms LD78-beta(3-70) and LD78-
 beta(3-70) are produced by proteolytic cleavage after LD78-
 from peripheral blood monocytes. The cleavage to yield LD78-
 beta(3-70) is probably achieved by DPP4.
 -I- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL: X52149; CAA36397.1; -; mRNA.
 CC EMBL: M24110; AAA35859.1; -; Genomic_DNA.

DR EMBL: D90145; BAAL1473.1; -; Genomic_DNA.
 DR EMBL: BC007783; AAH07783.1; -; mRNA.
 DR EMBL: BC027888; AAH27888.1; -; mRNA.
 DR PIR: B35673; B35673.
 DR HSSP: P10147; 1B50.
 DR SMR: P16619; 26-93.
 DR HGNC: HGNC:10628; CCL3L1.
 DR H-INDB: HIX0020418; -.
 DR H-INDB: HIX0023281; -.
 DR MIM: 601395; -.
 DR GO: GO:0005576; C:extracellular region; NAS.
 DR GO: GO:0008009; F:chemokine activity; NAS.
 DR GO: GO:0006935; P:chemotaxis; NAS.
 DR GO: GO:0006954; P:inflammatory response; TAS.
 DR InterPro: IPR000827; CC_chemokine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 KM Chemotaxis; Cytokine; Direct protein sequencing; Sensory transduction;
 FM Signal.
 FT CHAIN 1 23 Small inducible cytokine A3-like 1.
 FT CHAIN 24 93 LD78-beta(3-70).
 FT CHAIN 26 93 LD78-beta(5-70).
 FT SITE 28 93
 FT SITE 25 26 Cleavage (by DPP4) (probable).
 FT DISULFD 34 58 By similarity.
 FT DISULFD 35 74 By similarity.
 FT CONFLICT 91 91 L -> P (in Ref. 4; AAH07783).
 SQ SEQUENCE 93 AA; 10161 MW; A7A79E774006D61E CRC64;

 QY Query Match 52.4%; Score 218; DB 1; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

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 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

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 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

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 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
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 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
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 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
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 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
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 QY Query Match 52.4%; Score 218; DB 2; Length 93;
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 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
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 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
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 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

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 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 QY Query Match 52.4%; Score 218; DB 2; Length 93;
 Best Local Similarity 55.0%; Pred. No. 1.3e-16;
 Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 90

 DB 13 PSECCFTYTYKIPRQIRIMDYETNSQCKPGIVFTTRGHSVCTNPSPDKWQDYIKDKM 72
 31 PTAACFSYTSRQIPQNIADYFETISQCKSPSVIFLTRGRGVCAADPSEWQVKVSDLE 9

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RESULT 12
CC CCL4 RABIT STANDARD; PRT; 92 AA.
AC P4632;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).
GN Name=CCL4; Synonyms=SCYA4;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand white;
RX MEDLINE=94198229; PubMed=8148323;
RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156 (1994).
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties
(CC (By similarity)).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; D17402; BA004226.1; -; mRNA.
DR PIR; I46730; I46730.
DR HSSP; P13236; IHM.
DR SMR; P46632; 24-92.
DR InterPro; IPR000827; CC_chemokine_gml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00139; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KM Chemotaxis; Cytokine; Inflammatory response; Sensory transduction;
KM SIGNAL.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 92 Small inducible cytokine A4.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10066 MW; ECBA8818D42A735C CRC64;

Query Match 51.4%; Score 216; DB 1; Length 92;
Best local Similarity 50.0%; Pred. No. 2.1e-16;
Matches 35; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 5 SSSRGPHYBSCCPTTYTKIPRQINDYETNSQCSKPGIVFTTKGHSVCTNPSDKV 64
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 23 SAPGSDPPTACCSYTRKLPFRHFVIDYFETTSLSQPAVVVFOTKKGRVCANPSSWV 82
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 65 ODYIKDMKEN 74
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 83 QEYVDLELN 92

RESULT 13
Q4VSK4 ANAPL. PRT; 90 AA.
AC Q4VSK4 ANAPL PRELIMINARY;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)

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DR MIP-beta-like CC chemokine.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Amseriliformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mitogen stimulated spleen;
RX PubMed=15841394;
RA Sreekumar E., Premraj A., Arathy D.S., Raoool T.J.;
RT "Identification, sequence characterization, and analysis of expression
profiles of three novel CC chemokines from domestic duck (Anas
platyrhynchos).";
RL Immunogenetics 57:364-373 (2005).
DR EMBL; AY641437; AAV52797.1; -; mRNA.
DR NCBI_TaxID=9997 MW; 5B6FF22356423930 CRC64;
SQ SEQUENCE 90 AA; 9997 MW;

Query Match 51.4%; Score 214; DB 2; Length 90;
Best local Similarity 47.9%; Pred. No. 3.5e-16;
Matches 35; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 2 KTBSSRGPHYBSCCPTTYTKIPRQINDYETNSQCSKPGIVFTTKGHSVCTNPSD 61
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 18 QTSAPIGSDPPTACCSYTRKLPFRHFVIDYETNSLSKPGVVFITTKGHSVCTNPSD 77
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 62 KMWODYIKDMKEN 74
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 78 DWVKKYVTELELN 90

RESULT 14
Q68A20 CANPA PRELIMINARY; PRT; 92 AA.
AC Q68A20;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DB CC Chemokine ligand 4.
GN Name=CCL4;
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Teukui T., Sakaguchi M., Maeda S., Koyanagi M., Masuda K., Ohno K.,
RA Teukui T., Iwabuchi S.;
RT "Expression analysis of chemokine gene in canine atopic dermatitis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Teukui T., Maeda S., Koyanagi M., Hashimoto R., Masuda K., Ohno K.,
RA Sakaguchi M., Teukui M., Iwabuchi S.;
RT "Expression analysis of CCL4 gene in canine atopic dermatitis.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB163435; BAD37148.1; -; mRNA.
DR EMBL; AB163435; BAD37148.1; -; mRNA.
DR SMR; Q68A20; 24-92.
DR Ensembl; ENSCAGF00000018164; Canis familiaris.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_gml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00139; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10197 MW; 7628FBC425BED9C CRC64;

Query Match 51.4%; Score 214; DB 2; Length 92;
Best local Similarity 51.4%; Pred. No. 3.6e-16;
Matches 36; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

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QY 5 SSSRGYPHPSGCCFTYTYTKIPRQIRIMDYETNSQCSKPGIVFTTKGHSVCTNPSDKWV 64
 Db 23 SAPWGSPPPTACCSYTLRKIPRNFAVDYFETSSLCSPAVVQTRRGROYCANPSEBWV 82

QY 65 ODYIKDMKEN 74
 Db 83 QRYMDLELN 92

RESULT 15

CCL3_PANTR STANDARD; PRT; 92 AA.
 ID CCL3_PANTR
 AC Q51120;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha).
 DE Name=CCL3;
 GN Pan troglodytes (Chimpanzee).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
 NCBI_TaxID=9598;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed:15637236; DOI=10.1126/science.1101160;
 RA Gonzalez E., Kulikarni H., Bolivar H., Mangano A., Sanchez R., Carano G., Nibbs R.J., Freedman B.I., Quintones M.P., Bamehad M.J., Murthy K.K., Kovin B.H., Bradley W., Clark R.A., Anderson S.A., O'Connell R.D., Agan B.K., Ahuja S.S., Bologna R., Sen L., Dolan M.J., Ahuja S.K.;
 RA "The influence of CCL3L1 gene-containing segmental duplications on HIV-1/AIDS susceptibility".
 RL Science 307:1434-1440(2005).
 CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
 CC Binds to CCR1, CCR4 and CCR5 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL; AY864054; AAM57434.1; -, mRNA.
 DR SMR; Q51120; 24-92.
 DR InterPro; IPR000827; CC_chemokine_gml.
 DR InterPro; IPR01811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Chemotaxis; Cytokine; Inflammatory response; Sensory transduction; Signal.
 KM SIGNAL.
 FT CHAIN 1 23 By similarity.
 FT CHAIN 24 92 Small inducible cytokine A3.
 FT DISULFID 33 57 By similarity.
 FT DISULFID 34 73 By similarity.
 SQ SEQUENCE 92 AA; 10098 MW; 3DF0B8D5D677821 CRC64;
 Query Match 51.2%; Score 213; DB 1; Length 92;
 Best Local Similarity 50.0%; Pred. No. 4.6e-16;
 Matches 34; Conservative 17; Mismatches 17; Indels 0; Gaps 0;
 QY 5 SSSRGYPHPSGCCFTYTYTKIPRQIRIMDYETNSQCSKPGIVFTTKGHSVCTNPSDKWV 64
 Db 22 SASLADPTACCSYTLRKIPRNFAVDYFETSSLCSPKSPVIFLTRGROVCADPSEBWV 81
 QY 65 ODYIKDMK 72
 Db 82 QRYMDLE 89

Search completed: January 10, 2006, 22:59:19
 Job time : 161 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2006, 22:54:31 ; Search time 46 Seconds
(without alignments)
133,000 Million cell updates/sec

Title: US-10-760-557-6

Perfect score: 416
Sequence: 1 TKTSSSSGPHRPHSECCFTY.....VCTNPSDKMVDYIKDMKEN 74

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82655679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	416	100.0	93	1	US-08-173-209A-2
2	416	100.0	93	1	US-08-347-492B-6
3	416	100.0	93	1	US-08-798-143-6
4	416	100.0	93	2	US-08-722-719-2
5	416	100.0	93	2	US-09-180-077-7
6	416	100.0	93	2	US-09-334-951-2
7	416	100.0	93	2	US-09-334-923A-2
8	416	100.0	93	2	US-09-334-954A-2
9	416	100.0	93	2	US-09-834-795A-30
10	416	100.0	93	2	US-09-571-013-2
11	416	100.0	93	4	PCT-US95-15484-6
12	405	97.4	72	2	US-09-567-225-1
13	394	94.7	109	2	US-09-180-077-12
14	328	54.8	86	1	US-08-421-144A-9
15	219	52.6	72	1	US-08-330-163-13
16	219	52.6	72	1	US-08-482-111-13
17	219	52.6	92	1	US-07-792-988-1
18	219	52.6	92	1	US-08-347-492B-10
19	219	52.6	92	1	US-08-375-346A-3
20	219	52.6	92	1	US-08-230-574-2
21	219	52.6	92	1	US-08-480-449-23
22	219	52.6	92	1	US-08-633-682-4
23	219	52.6	92	1	US-08-421-144A-3
24	219	52.6	92	1	US-08-660-542-23
25	219	52.6	92	1	US-08-535-116-3
26	219	52.6	92	1	US-08-598-143-10
27	219	52.6	92	1	US-08-467-123B-3

28	219	52.6	92	2	US-08-722-719-53	Sequence 53, Appl
29	219	52.6	92	2	US-08-936-772-4	Sequence 4, Appl
30	219	52.6	92	2	US-08-808-720-9	Sequence 9, Appl
31	219	52.6	92	2	US-09-395-918-4	Sequence 4, Appl
32	219	52.6	92	2	US-09-133-521-7	Sequence 7, Appl
33	219	52.6	92	2	US-08-679-493A-161	Sequence 161, App
34	219	52.6	92	2	US-08-479-603-23	Sequence 23, Appl
35	219	52.6	92	2	US-09-334-951-53	Sequence 53, Appl
36	219	52.6	92	2	US-09-334-923A-53	Sequence 36, Appl
37	219	52.6	92	2	US-09-689-693-16	Sequence 36, Appl
38	219	52.6	92	2	US-08-939-107-23	Sequence 23, Appl
39	219	52.6	92	2	US-09-151-450-3	Sequence 3, Appl
40	219	52.6	92	2	US-09-334-954A-53	Sequence 53, Appl
41	219	52.6	92	2	US-09-834-795A-33	Sequence 33, Appl
42	219	52.6	92	2	US-09-467-638-9	Sequence 9, Appl
43	219	52.6	92	2	US-09-067-447B-23	Sequence 23, Appl
44	219	52.6	92	2	US-08-479-620-23	Sequence 23, Appl
45	219	52.6	92	2	US-09-571-013-55	Sequence 55, Appl

ALIGNMENTS

SEQUENCE COMPARISON A

RESULT 1
US-08-173-209A-2
Sequence 2, Application US/08173209A
Patent No. 5556767
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Macrophage Inflammatory Protein Gamma
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173, 209A
FILING DATE: 22 DECEMBER 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-51
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: LINEAR
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-173-209A-2
Query Match 100.0%; Score 416; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.4e+43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TKTSSSSGPHRPHSECCFTYTYTKIPRORIMDYETNSQCSKPGIVITKRGHSVCTNPS 60
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Db 20 TKTESSRGPHBSECFTYTYTKIPRORIMDYETNSQCSKPGIVITRKHSVCTNPS 79
QY 61 |||||
Db 80 DKWVDYIKMKEN 93

RESULT 2
US-08-347-492B-6
Sequence 6, Application US/08347492B
Patent No. 5602008
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRES:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: PITUITARY
CLONE: 115571
US-08-347-492B-6

Query Match 100.0%; Score 416; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 3,4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TKTESSRGPHBSECFTYTYTKIPRORIMDYETNSQCSKPGIVITRKHSVCTNPS 60
Db 20 TKTESSRGPHBSECFTYTYTKIPRORIMDYETNSQCSKPGIVITRKHSVCTNPS 79
QY 61 DKWVDYIKMKEN 74
Db 80 DKWVDYIKMKEN 93

RESULT 3
US-08-798-143-6

Sequence 6, Application US/08798143
Patent No. 5936068
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,143
FILING DATE: 10-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,492
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: PITUITARY
CLONE: 115571
US-08-798-143-6

Query Match 100.0%; Score 416; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 3,4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TKTESSRGPHBSECFTYTYTKIPRORIMDYETNSQCSKPGIVITRKHSVCTNPS 60
Db 20 TKTESSRGPHBSECFTYTYTKIPRORIMDYETNSQCSKPGIVITRKHSVCTNPS 79
QY 61 DKWVDYIKMKEN 74
Db 80 DKWVDYIKMKEN 93

RESULT 4
US-08-722-719-2
Sequence 2, Application US/08722719
Patent No. 6001606
GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
APPLICANT: RUBIN, STEVEN M.
APPLICANT: LI, HAODONG

APPLICANT: ADAMS, MARK D.
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR
TREATING DISEASE STATES WITH MYELOID PROGENITOR INHIBITORY
TITLE OF INVENTION: TREATING DISEASE STATES WITH MYELOID PROGENITOR INHIBITORY
TITLE OF INVENTION: FACTOR-1 (MPF-1), MONOCYTE COLONY INHIBITORY FACTOR
TITLE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR-4 (MIP-4)
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KASSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,719
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,209
FILING DATE: 22-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,339
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,881
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,682
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,775
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0330007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-719-2

Query Match 100.0%; Score 416; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGPYPHSPSCCTTTTYYKIPRORIMDYETNSGCKRGIVFTTKRGHSVCTNPS 60
DB 20 TKTSSSRGPYPHSPSCCTTTTYYKIPRORIMDYETNSGCKRGIVFTTKRGHSVCTNPS 79

QY 61 DKWVDYIKDMKEN 74
DB 80 DKWVDYIKDMKEN 93

RESULT 5
US-09-180-077-7
Sequence 7, Application US/09180077A
Patent No. 6180773
GENERAL INFORMATION:
APPLICANT: Forsmann, Wolf-Georg
APPLICANT: Pardigol, Andreas
APPLICANT: Megett, Hans-Jurgen

APPLICANT: Schulz-Knappe, Peter
TITLE OF INVENTION: NEW CC TYPE CHEMOKINES
FILE REFERENCE: 10496/B63140USO
CURRENT APPLICATION NUMBER: US/09/180,077A
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: PCT/EP97/02217
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: DE 196 17 312.4
EARLIER FILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-077-7

Query Match 100.0%; Score 416; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGPYPHSPSCCTTTTYYKIPRORIMDYETNSGCKRGIVFTTKRGHSVCTNPS 60
DB 20 TKTSSSRGPYPHSPSCCTTTTYYKIPRORIMDYETNSGCKRGIVFTTKRGHSVCTNPS 79

QY 61 DKWVDYIKDMKEN 74
DB 80 DKWVDYIKDMKEN 93

RESULT 6
US-09-334-951-2
Sequence 2, Application US/09334951
Patent No. 6451562
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
APPLICANT: Li, Haodong
TITLE OF INVENTION: Myeloid Progenitor Inhibitory Factor-1 (MPF-1)
FILE REFERENCE: 1488.033000B
CURRENT APPLICATION NUMBER: US/09/334,951
CURRENT FILING DATE: 1999-06-17
EARLIER APPLICATION NUMBER: US 08/208,339
EARLIER FILING DATE: 1994-03-08
EARLIER APPLICATION NUMBER: US 08/446,881
EARLIER FILING DATE: 1995-05-05
EARLIER APPLICATION NUMBER: US 08/465,682
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: US 08/468,775
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: US 08/722,719
EARLIER FILING DATE: 1996-09-30
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
US-09-334-951-2

Query Match 100.0%; Score 416; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGPYPHSPSCCTTTTYYKIPRORIMDYETNSGCKRGIVFTTKRGHSVCTNPS 60
DB 20 TKTSSSRGPYPHSPSCCTTTTYYKIPRORIMDYETNSGCKRGIVFTTKRGHSVCTNPS 79

QY 61 DKWVDYIKDMKEN 74
DB 80 DKWVDYIKDMKEN 93

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RESULT 7
US-09-334-923A-2
; Sequence 2, Application US/09334923A
; Patent No. 648925
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Macrophage Inflammatory Protein-4 (MIP-4) Polypeptides (As Amended)
; FILE REFERENCE: 1488.033000D
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 08/208,339
; PRIOR FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: US 08/446,881
; PRIOR FILING DATE: 1995-05-05
; PRIOR APPLICATION NUMBER: US 08/465,682
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/468,775
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/722,719
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-334-923A-2

Query Match      100.0%; Score 416; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3,4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCSKPGIVFTYRKGHSVCTNPS 60
Db 20 TKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCSKPGIVFTYRKGHSVCTNPS 79
QY 61 DKWVDYIKDMKEN 74
Db 80 DKWVDYIKDMKEN 93

RESULT 8
US-09-334-954A-2
; Sequence 2, Application US/09334954A
; Patent No. 6623942
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Macrophage Inflammatory Protein-4 (MIP-4) Polynucleotides
; FILE REFERENCE: 1488.033000C
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 08/208,339
; PRIOR FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: US 08/446,881
; PRIOR FILING DATE: 1995-05-05
; PRIOR APPLICATION NUMBER: US 08/465,682
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/468,775
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/722,719
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-334-954A-2

Query Match      100.0%; Score 416; DB 2; Length 93;
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Best Local Similarity 100.0%; Pred. No. 3,4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCSKPGIVFTYRKGHSVCTNPS 60
Db 20 TKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCSKPGIVFTYRKGHSVCTNPS 79
QY 61 DKWVDYIKDMKEN 74
Db 80 DKWVDYIKDMKEN 93

RESULT 9
US-09-834-795A-30
; Sequence 30, Application US/09834795A
; Patent No. 6723518
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papeidero
; APPLICANT: Lyn, Dyster
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/1127-US3
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
; PRIOR FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-795A-30

Query Match      100.0%; Score 416; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3,4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCSKPGIVFTYRKGHSVCTNPS 60
Db 20 TKTSSSRGYPHPSECCFTYTYTKIPRQIMDYETNSQCSKPGIVFTYRKGHSVCTNPS 79
QY 61 DKWVDYIKDMKEN 74
Db 80 DKWVDYIKDMKEN 93

RESULT 10
US-09-571-013-2
; Sequence 2, Application US/09571013
; Patent No. 6811773
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER L.
; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR
; TREATING DISEASE STATES WITH MYELOID PROGENITOR INHIBITORY
; FACTOR-1 (MPLF-1), MONOCYTE COLONY INHIBITORY FACTOR
; (M-CIF), AND MACROPHAGE INHIBITORY FACTOR-4 (MIP-4)
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/571,013
FILING DATE: 15-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/941,020
FILING DATE: 30-SEP-1997
APPLICATION NUMBER: US 60/027,299
FILING DATE: 30-SEP-1996
APPLICATION NUMBER: US 60/027,300
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0330009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-571-013-2

*Query Match 100.0%; Score 416; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGPPHPSGCCFTYTTTKIPRQIMDYETNSQSKPGIVFTKRGHSVCTNPS 60
DB 20 TKTSSSRGPPHPSGCCFTYTTTKIPRQIMDYETNSQSKPGIVFTKRGHSVCTNPS 79

QY 61 DKWVDYIKDMKEN 74
DB 80 DKWVDYIKDMKEN 93

RESULT 11
PCT-US95-15484-6
Sequence 6, Application PC/TUS9515484
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR PRODUCTION AND
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15484
FILING DATE: 29-NOV-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,492
FILING DATE: 29-NOV-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J
REGISTRATION NUMBER: 33954

REFERENCE/DOCKET NUMBER: PF-0024 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Plutitary gland
CLONE: 111571
PCT-US95-15484-6

*Query Match 100.0%; Score 416; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.4e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGPPHPSGCCFTYTTTKIPRQIMDYETNSQSKPGIVFTKRGHSVCTNPS 60
DB 20 TKTSSSRGPPHPSGCCFTYTTTKIPRQIMDYETNSQSKPGIVFTKRGHSVCTNPS 79

QY 61 DKWVDYIKDMKEN 74
DB 80 DKWVDYIKDMKEN 93

RESULT 12
US-09-567-225-1
Sequence 1, Application US/09567225
Patent No. 6713052
GENERAL INFORMATION:
APPLICANT: White, John R.
APPLICANT: Pelus, Louis
APPLICANT: Li, Haodong
APPLICANT: Kreider, Brent L.
TITLE OF INVENTION: No. 6713052el Chemokine for Mobilizing Stem Cells
FILE REFERENCE: 1488.1550004
CURRENT APPLICATION NUMBER: US/09/567,225
CURRENT FILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: US 09/225,501
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: US 60/006,051
PRIOR FILING DATE: 1995-10-24
PRIOR APPLICATION NUMBER: US 08/740,033
PRIOR FILING DATE: 1996-10-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 72
TYPE: PRT
ORGANISM: CKBeta-1
US-09-567-225-1

*Query Match 97.4%; Score 405; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKTSSSRGPPHPSGCCFTYTTTKIPRQIMDYETNSQSKPGIVFTKRGHSVCTNPS 60
DB 1 TKTSSSRGPPHPSGCCFTYTTTKIPRQIMDYETNSQSKPGIVFTKRGHSVCTNPS 60

QY 61 DKWVDYIKDMK 72
DB 61 DKWVDYIKDMK 72

RESULT 13
US-09-180-077-12
Sequence 12, Application US/09180077A
Patent No. 6180773

Fr1 Jan 13 11:59:20 2006

us-10-760-557-6.ra

Page 6

```

: GENERAL INFORMATION:
: APPLICANT: Forssmann, Wolf-Georg
: APPLICANT: Pardigol, Andreas
: APPLICANT: Magerl, Hans-Jürgen
: APPLICANT: Schultz-Knappe, Peter
: TITLE OF INVENTION: NEW CC TYPE CHEMOKINES
: FILE REFERENCE: 10496/P63140USO
: CURRENT APPLICATION NUMBER: US/09/180,077A
: CURRENT FILING DATE: 1998-12-30
: EARLIER APPLICATION NUMBER: PCT/EP97/02217
: EARLIER FILING DATE: 1997-04-30
: EARLIER APPLICATION NUMBER: DE 196 17 312.4
: EARLIER FILING DATE: 1996-04-30
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 12
: LENGTH: 109
: TYPE: PRT
: ORGANISM: Homo sapiens
: OS-09-180-077-12

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Query Match	94.7%	Score 394	DB 2	Length 109
Best Local Similarity	81.1%	Pred. No. 2e-40	0	Indels 16
Matches 73	Conservative 1	Mismatches 0	Indels 16	Gaps 1
QY	1	TKTSSSR-----	GPYHSRCCFTYTTYYKIPRORIMDYETNSOCSKPG	44
Db	20	TKTSSSRQTGAKPRVYKIQLKLVGGPYHPSRCCFTYTTYYKIPRORIMDYETNSOCSKPG		79
QY	45	IVFTTKRGHSVCTNPSDKMVDYIKDMKEN		74
Db	80	IVFTTKRGHSVCTNPSDKMVDYIKDMKEN		109

```

1      RESULT 14
2      US-08-421-144A-9
3      Sequence 9, Application US/08421144A
4      Patent No. 5874211
5      * GENERAL INFORMATION:
6      APPLICANT: BANDMAN, OLGA
7      APPLICANT: COLEMAN, ROGER
8      APPLICANT: STUART, SUSAN G.
9      TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
10     NUMBER OF SEQUENCES: 9
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
13     STREET: 3174 Porter Drive
14     CITY: Palo Alto
15     STATE: CA
16     COUNTRY: USA
17     ZIP: 94304
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: PatentIn Release #1.0, Version #1.30
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/421,144A
25     FILING DATE: 13-APR-1995
26     CLASSIFICATION: 435
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Luther, Barbara J.
29     REGISTRATION NUMBER: 33954
30     REFERENCE/DOCKET NUMBER: PF-0031 US
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: 415-855-0555
33     TELEFAX: 415-852-0195
34     INFORMATION FOR SEQ ID NO: 9:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 86 amino acids
37     TYPE: amino acid
38     STRANDEDNESS: single
39     TOPOLOGY: linear

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US-08-421-144A-9	MOLECULE TYPE: protein
Query Match	54.8%; Score 228; DB 1; length 86;
Best Local Similarity	64.9%; Pred. No. 2.5e-20;
Matches 37; Conservative 10; Mismatches 10; Indels 0; Gaps 0;	
13 PSECCFTYYTYKIPRQIRIMDYETNSQCSKPGIVFTIKRGHSVCTNFSKXWVDYIK 69	
22 PTTCCSFYINRKIKIPRCLSESYFETSSQCSKPAVIFKTRKGEVADSEKXWVDYIK 78	

RESULT 15
 US-08-330-163-13
 : Sequence 13, Application US/08330163
 : Patent No. 5656724
 :
 : GENERAL INFORMATION:
 : APPLICANT: Daly, Thomas J.
 : APPLICANT: Larosa, Gregory J.
 : TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
 : TITLE OF INVENTION: Use
 : NUMBER OF SEQUENCES: 46
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fish & Richardson
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: MA
 :
 : COUNTRY: U.S.A.
 : ZIP: 02110-2804
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.30B
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/330.163
 : FILING DATE: 05-AUG-1994
 :
 : CLASSIFICATION: 530
 :
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Faase, J. Peter
 : REGISTRATION NUMBER: 32,983
 : REFERENCE/DOCKET NUMBER: 00231/080001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (617) 542-5070
 : TELEFAX: (617) 542-8906
 :
 : INFORMATION FOR SEQ ID NO: 13:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 72 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 :
 : MOLECULE TYPE: peptide
 :
 : US-08-330-163-13

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Query Match      52.6% Score 219; DB 1: Length 72;  
Beat Local Similarity   51.5%; Pred No 2, Se-19;  
Matches          35; Conservative    17; Mismatches     16; Indels       0; Gaps        0,  
  
QY      5 SSSAGPYPHPSECCCTTTTYYTKIPRORIDNDYYETNSQCSPGIVFTTRKGHSVCTNPSDCKV 64  
Db      2 SASLADLPPTACCSFSTYSKROIPLONFIADVIFETSQSCKPGVIFLTRKSROYCADPDSBKW 61  
           |||||:::||:  
QY      65 QDYIKDMK 72  
           |::|  
Db      62 QRKYVDLE 69
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Search completed: January 10, 2006, 23:01:07
Job time : 47 secs

Search completed: January 10, 2006, 23:01:07
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2006, 22:52:16 ; Search time 38 Seconds
(without alignments)
187.369 Million cell updates/sec

Title: US-10-760-557-6

Perfect score: 416
Sequence: 1 TKTESSSRGPRHSECCFTY.....VCTNPDKWQDYIKMKEN 74

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	219	52.6	92	2	A30574	macrophage inflamm
2	218	52.4	92	2	C30552	macrophage inflamm
3	218	52.4	93	2	B35673	LD78-beta protein
4	216	51.9	92	2	I46730	immune activation
5	212	51.0	92	2	A31767	macrophage inflamm
6	200.5	48.2	92	2	A33393	macrophage inflamm
7	191.5	46.0	92	2	I53322	macrophage inflamm
8	172	41.3	91	1	A28815	monocyte chemotatr
9	167	40.1	91	1	A45339	monocyte chemotatr
10	163.5	39.3	120	2	UE0177	lymphocyte and non
11	163	39.2	50	2	C60407	monocyte adherence
12	157.5	37.9	116	2	I49555	gene C10 protein -
13	150.5	36.2	148	1	A30209	PDGF-inducible JB
14	145.5	35.0	99	2	JC5295	monocyte chemotatr
15	145.5	35.0	148	1	S07723	immediate-early se
16	144	34.6	99	2	UC1336	monocyte chemotatr
17	139.5	33.5	125	2	I46857	monocyte chemotatr
18	138.5	33.3	109	2	A54678	monocyte chemotatr
19	136	32.7	99	1	A39296	monocyte chemotatr
20	136	32.7	99	2	JC2336	monocyte chemotatr
21	128.5	30.9	97	2	JC4912	eotaxin precursor
22	127.5	30.6	99	2	JC2417	monocyte chemotatr
23	126	30.3	120	2	I48147	monocyte chemotatr
24	123.5	29.7	96	2	JC2478	eotaxin precursor
25	123.5	29.7	96	2	I48099	eotaxin precursor
26	122.5	29.4	99	2	A60299	monocyte chemotatr
27	122	29.3	72	2	A55984	monocyte chemotatr
28	119	28.6	96	2	A37236	I-309 protein prec
29	113	27.2	114	1	ETHUL	lymphotactin precu

30	107.5	25.8	97	2	A48093	monocytic cytokine
31	92	22.1	114	1	ETMSL	lymphotactin precu
32	86.5	20.8	92	2	S24236	TC43 protein - mou
33	77.5	18.6	95	2	JN0841	interleukin-8 - do
34	75.5	18.1	101	2	S42496	interleukin-8 - ra
35	71.5	17.2	101	2	I46871	interleukin-8 - ra
36	71	17.1	103	2	A53096	interleukin-8 prec
37	68.5	16.5	103	2	I50417	RSV-induced proteol
38	68.5	16.5	103	2	A26736	transformation-ind
39	68.5	16.5	311	2	T23873	hypothetical prote
40	68.5	16.5	316	2	H90372	catechol 2,3-dioxy
41	66	15.9	101	2	I48148	Neutrophil attract
42	66	15.9	942	2	T19553	hypothetical prote
43	65	15.6	348	2	T03911	r40c1 protein - ri
44	64.5	15.5	99	2	A37034	interleukin-8 prec
45	63.5	15.3	461	1	A35356	tumor necrosis fac

ALIGNMENTS

RESULT 1
A30574
macrophage inflammatory protein 1-alpha precursor - human
N:Alternate names: LD78-alpha protein precursor; lymphocyte tumor promoter-induced protei
tivation protein 1
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C:Accession: A30574; A30574; A30412; A24198; A30908
R:Nakao, M.; Nomiya, H.; Shimada, K.
Mol. Cell. Biol. 10, 3646-3658, 1990
A:Title: Structures of human genes coding for cytokine LD78 and their expression.
A:Reference number: A30573; MUID:90287155; PMID:1694014
A:Accession: A30574
A:Molecule type: DNA
A:Residues: 1-92 <NAK>
A:Cross-references: UNIPROT:P10147; UNIPARC:UPI00001362C9; GB:D90144; NID:9219905; PIDN:F
R:Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.
U. Immunol. 142, 1582-1590, 1989
A:Title: Mitogenic activation of human T cells induces two closely related genes which sh
A:Reference number: A30574; MUID:89140347; PMID:2521882
A:Accession: A30574
A:Molecule type: mRNA
A:Residues: 1-92 <ZIP>
A:Cross-references: UNIPARC:UPI00001362C9; GB:M25315; NID:9602452; PIDN:AAA57255.1; PID:G
R:Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.
DNA Cell Biol. 9, 589-602, 1990
A:Title: Three human homologs of a murine gene encoding an inhibitor of stem cell prolif
A:Reference number: A30412; MUID:91103879; PMID:2271120
A:Accession: A30412
A:Molecule type: mRNA
A:Residues: 1-92 <BLU>
A:Cross-references: UNIPARC:UPI00001362C9; GB:M23178; GB:M32337; NID:9182846; PIDN:AAA35
R:Obaru, K.; Fukuda, M.; Maeda, S.; Shimada, K.
J. Biochem. 99, 885-894, 1986
A:Title: A cDNA clone used to study mRNA inducible in human tonsillar lymphocytes by a tr
A:Reference number: A24198; MUID:86223879; PMID:3086300
A:Accession: A24198
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <OBA>
A:Cross-references: UNIPARC:UPI00001362C9; GB:X03754; NID:934298; PIDN:CAA27388.1; PID:G
C:Gene: GDB:SCYA3
A:Cross-references: GDB:120368; OMIM:182283
A:Map position: 17q11-17q21
C:Superfamily: macrophage inflammatory protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-92/Product: macrophage inflammatory protein 1-alpha #status predicted <MAT>
F:33-57,34-73/Disulfide bonds: #status predicted

Query Match 52.6%; Score 219; DB 2; Length 92;
Best Local Similarity 51.5%; Pred. No. 1.5e-17;

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Matches 35; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
QY 5 SSSRGPHPSBCCFTYTYTKIPRORIMDYETNSQCSKPGIVFITKRGHSVCTNPSDKWV 64
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 22 SASLADLPTRKCCFTYSRQIPQNFADYFETSSQCSKPGIVFITKRGHSVCTNPSDKWV 81
QY 65 ODYIKDMK 72
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 82 OKYVSDLE 89

RESULT 2
macrophage inflammatory protein 1-beta precursor - mouse
N:Alternate names: H400; SIS gamma; T-cell activation protein gamma
C:Species: Mus musculus (house mouse)
C>Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
C/Accession: C30552; J10088; F50304; S22042
C/Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J:Immunol. 142, 679-687, 1989
A:Title: A family of small inducible proteins secreted by leukocytes are members of a new family of various activation processes.
A:Reference number: A30552; MUID:89093958; PMID:2521353
A/Accession: C30552
A/Molecule type: mRNA
A/Residues: 1-92 <BRO>
A/Cross-references: UNIPROT:P14097; UNIPARC:UP1000000293; GB:M23503; NID:G533244; PIDN:
J:Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mac
J:Exp. Med. 168, 2251-2259, 1988
A:Title: Resolution of the two components of macrophage inflammatory protein 1, and clon
A:Reference number: J10088; MUID:89067830; PMID:3058856
A/Accession: J10088
A/Molecule type: mRNA
A/Residues: 1-92 <SHS>
A/Cross-references: UNIPARC:UP1000000293; GB:M35590; NID:G199696; PIDN:AAA39708.1; PID:
A/Accession: F50304
A/Molecule type: protein
A/Residues: 24-33/'XX',36,'X',38 <SH2>
A/Cross-references: UNIPARC:UP10000176746
C:Substrates, P.; Lepetier, F.; Baillet, B.; Grove, M.; Pragnell, I.; Plumb, M.
Submitted to the EMBL Data Library, October 1991
A/Description: Sequence of the murine macrophage inflammatory protein 1b gene.
A/Reference number: S22042
A/Accession: S22042
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-92 <DAD>
A/Cross-references: UNIPARC:UP1000000293; EMBL:X62502; NID:G53126; PIDN:CAA44364.1; PII
C/Comment: This protein is a monokine.
C/Genetics:
A/Intons: 26/1; 64/2
C/Superfamily: macrophage inflammatory protein
C/Keywords: glycoprotein
F:1.23/Domain: signal sequence #status predicted <SIG>
F:24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.4%; Score 218; DB 2; Length 92;
Best Local Similarity 50.0%; Pred. No. 1.9e-17;
Matches 35; Conservative 16; Mismatches 19; Indels 0; Gaps 0;
QY 5 SSSRGPHPSBCCFTYTYTKIPRORIMDYETNSQCSKPGIVFITKRGHSVCTNPSDKWV 64
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Db 23 SAPMGSDPPTSCFTYSRQHRFVMDYETSSILCSKPAVAVFITKRGROICAMPSEBFW 82
QY 65 ODYIKDMKEN 74
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 83 TEWMSDLEIN 92

RESULT 3
LD78-beta protein precursor - human
```

```
N:Alternate names: macrophage inflammatory protein homolog GOS19-2; small inducible cyto
C:Species: Homo sapiens (man)
C>Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 09-Jul-2004
C/Accession: B35673; B30412; G10157; B30908
C/Brown, K.; Nishiyama, H.; Shimada, K.
Mol. Cell. Biol. 10, 3646-3658, 1990
A:Title: Structures of human genes coding for cytokine LD78 and their expression.
A:Reference number: A35673; MUID:9028715; PMID:1694014
A/Accession: B35673
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-93 <NAK>
A/Cross-references: UNIPROT:P16619; UNIPARC:UP1000004457D; GB:D90145; NID:G219907; PIDN:
R:Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.
DNA Cell Biol. 9, 589-602, 1990
A:Title: Three human homologs of a murine gene encoding an inhibitor of stem cell prolif
A/Reference number: A30412; MUID:9103879; PMID:2271120
A/Accession: B30412
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-93 <BLU>
A/Cross-references: UNIPARC:UP100004457D; GB:M24110; GB:M32338; NID:G182848; PIDN:AAA35
R:Irving, S.G.; Zipefel, P.F.; Balke, J.; McBride, O.W.; Morton, C.C.; Bird, P.R.; Siebenl
Nucleic Acids Res. 18, 3261-3270, 1990
A:Title: Two inflammatory mediator cytokine genes are closely linked and variably amplifi
A/Reference number: S10157; MUID:90287702; PMID:1972563
A/Accession: S10157
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-93 <IRV>
A/Cross-references: UNIPARC:UP100004457D; EMBL:X52149; NID:G34750; PIDN:CAA36397.1; PID:
C/Comment: This protein is a member of a "small inducible" or "activation specific" gene
C/Genetics:
A/Gene: GDB:SCY44
A/Cross-references: GDB:120369; OMIM:182284
A/Map position: 17q11-17q21
A/Intons: 26/1; 64/2
C/Superfamily: macrophage inflammatory protein
C/Keywords: cytokine
F:1.22/Domain: signal sequence #status predicted <SIG>
F:23-93/Product: LD78-beta protein #status predicted <MAT>

Query Match 52.4%; Score 218; DB 2; Length 93;
Best Local Similarity 55.0%; Pred. No. 1.9e-17;
Matches 33; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
QY 13 PSBCCFTYTYTKIPRORIMDYETNSQCSKPGIVFITKRGHSVCTNPSDKWVODYIKDMK 72
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 PTACCFYSYTSRQIPQNFADYFETSSQCSKPGIVFITKRGHSVCTNPSDKWVOKYVSDLE 90

RESULT 4
immune activation gene 2 - rabbit
146730
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C/Accession: 146730
C/Mori, S.; Goto, K.; Goto, F.; Mutakami, K.; Ohkawara, S.; Yoshinaga, M.
Int. Immunol. 6, 149-156, 1994
A:Title: Dynamic changes in mRNA expression of neutrophils during the course of acute in
A/Reference number: 146730; MUID:94198229; PMID:8148323
A/Accession: 146730
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-92 <MOR>
A/Cross-references: UNIPROT:P46632; UNIPARC:UP100001362CD; GB:D17402; NID:G599577; PIDN:
C/Superfamily: macrophage inflammatory protein

Query Match 51.9%; Score 216; DB 2; Length 92;
Best Local Similarity 50.0%; Pred. No. 3.2e-17;
Matches 35; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
QY 5 SSSRGPHPSBCCFTYTYTKIPRORIMDYETNSQCSKPGIVFITKRGHSVCTNPSDKWV 64
```

Db 23 SAPMSDPPTACCTSYTRKLPKRPVVDYETSLCSQPAVVFQTKRGKQVCANPSESVM 82
QY 65 QDYIKMKEN 74
Db 83 QEVYDDLELN 92

RESULT 5
A31767
macrophage inflammatory protein 1-beta precursor [validated] - human
N:Alternate names: cytokine HC21; G-26 protein; H400 homolog; lymphocyte activation gene
protein 2 (Act-2); T-cell activation protein gamma
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence revision 29-May-1998 #text change 09-Jul-2004
C:Accession: J00319; A40978; A31767; A37411; B30574; B45817; D30552
R:Napolitano, M.; Modi, W.S.; Cevallo, S.J.; Gnattar, J.R.; Senanez, H.N.; Leonard, W.J.
J. Biol. Chem. 266, 17531-17536, 1991
A:Title: The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/tax responsiveness
Mol. Immunol. 27, 1091-1102, 1990
A:Title: Cloning and expression of a lymphocyte activation gene (LAG-1).
A:Reference number: J00319; MUID:91061800; PMID:2247088
A:Accession: J00319
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-92 <BAI>
A:Cross-references: UNIPROT:P13336; UNIPARC:UPI00001362CC; GB:X53682; NID:934217; PIDN:C
A:Experimental source: natural killer cell, strain CD3-CD24, F5, SITES
R:Napolitano, M.; Modi, W.S.; Cevallo, S.J.; Gnattar, J.R.; Senanez, H.N.; Leonard, W.J.
J. Biol. Chem. 266, 17531-17536, 1991
A:Title: The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/tax responsiveness
A:Reference number: A40978; MUID:91373378; PMID:1894635
A:Accession: A40978
A:Molecule type: DNA
A:Residues: 1-14, 'S', 16-69, 'G', 71-92 <NAP>
A:Cross-references: UNIPARC:UPI000016A493; GB:M69201; NID:9178021
M:Note: 15-Ala was also found
R:Lopes, M.A.; Napolitano, M.; Jeang, K.T.; Chang, N.T.; Leonard, W.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 9704-9708, 1988
A:Title: Identification, cloning, and characterization of an immune activation gene.
A:Reference number: A31767; MUID:89071764; PMID:2462251
A:Accession: A31767
A:Molecule type: mRNA
A:Residues: 1-92 <LIP>
A:Cross-references: UNIPARC:UPI00001362CC; GB:J04130; NID:9178017; PIDN:AAA51576.1; PID:
R:Chang, H.C.; Reinherz, E.L.
Eur. J. Immunol. 19, 1045-1051, 1989
A:Title: Isolation and characterization of a cDNA encoding a putative cytokine which is
A:Reference number: A37411; MUID:89325421; PMID:2568930
A:Accession: A37411
A:Molecule type: mRNA
A:Residues: 1-92 <CHA>
A:Cross-references: UNIPARC:UPI00001362CC; GB:X16166; NID:932035; PIDN:CAA34291.1; PID:G
R:Ziffler, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.
J. Immunol. 142, 1582-1590, 1989
A:Title: Mitogenic activation of human T cells induces two closely related genes which
A:Reference number: A30574; MUID:89140347; PMID:2521882
A:Accession: B30574
A:Molecule type: mRNA
A:Residues: 1-19, 'T', 21-92 <ZIP>
A:Cross-references: UNIPARC:UPI000016A787; GB:M25316; NID:9602454; PIDN:AAA57256.1; PID:
R:Miller, M.D.; Hara, S.; Malefey, R.D.W.; Krangel, M.S.
J. Immunol. 143, 2907-2916, 1989
A:Title: A novel polypeptide secreted by activated human T lymphocytes.
A:Reference number: A45817; MUID:90038522; PMID:2809212
A:Accession: B45817
A:Molecule type: mRNA
A:Residues: 7-55, 'T', 57-79, 'T', 81-92 <MTL>
A:Cross-references: UNIPARC:UPI00001736A0; GB:M57503; NID:9339726; PIDN:AAA6752.1; PID:
R:Brown, K.D.; Zurawski, S.M.; Kosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1989
A:Title: A family of small inducible proteins secreted by leukocytes are members of a ne
s of various activation processes.
A:Reference number: A30552; MUID:89093958; PMID:2521353
A:Accession: D30552

A:Molecule type: mRNA
A:Residues: 1-39, 'REASS', 46-92 <BRO>
A:Cross-references: UNIPARC:UPI0000147059; GB:M23502; NID:9533212; PIDN:AAA6656.1; PID:S
R:Clote, G.M.; Lodi, P.J.; Garrett, D.S.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1994
A:Reference number: A52206; PDB:1HOM
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues
C:Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound t
C:Genetics:
A:Gene: GDB:LMG1
A:Cross-references: GDB:127451; OMIM:153335
A:Map position: 17q21-17q21
A:Introns: 26/1; 64/2
C:Superfamily: macrophage inflammatory protein
C:Keywords: chemotaxis; cytokine; inflammation
F:1-33/Domain: signal sequence #status predicted <SIG>
F:24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
F:34-58,35-74/Distulfide bonds: #status experimental

Query Match 51.0%; Score 212; DB 1; Length 92;
Best Local Similarity 50.0%; Pred. No. 9e-17;
Matches 35; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 5 SSSRGPPYRSECCTTYTYKIPRQIRINDYETNSQSRKGIYFTTKRGHSVCTNPSEKXV 64
Db 23 SAPMSDPPTACCTSYTRKLPKRPVVDYETSLCSQPAVVFQTKRGKQVCANPSESVM 82

QY 65 QDYIKMKEN 74
Db 83 QEVYDDLELN 92

RESULT 6
A23393
macrophage inflammatory protein-1-alpha precursor - mouse
N:Alternate names: heparin-binding chemotaxis protein; LZG25B protein; SCI/MIP-1a; SIS a)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text change 09-Jul-2004
C:Accession: S11685; A32393; S04533; A53885; A30552; P80303; A27596; I56104
R:Grove, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M.
Nucleic Acids Res. 18, 5561, 1990
A:Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammatory
A:Reference number: S11685; MUID:91016858; PMID:2216738
A:Accession: S11685
A:Molecule type: DNA
A:Residues: 1-92 <GRO>
A:Cross-references: UNIPROT:P10855; UNIPARC:UPI000020B06; EMBL:X53372; NID:954062; PIDN:
A:Note: the authors' translation of the nucleotide sequence differs at several positions
R:Kwon, B.S.; Weisman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A:Title: cDNA sequence of two inducible T-cell genes.
A:Reference number: A23393; MUID:89184547; PMID:2784565
A:Accession: A23393
A:Molecule type: mRNA
A:Residues: 1-92 <OMO>
A:Cross-references: UNIPARC:UPI000020B06; GB:J04491; NID:9201524; PIDN:AAA40304.1; PID:C
R:Davidellis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.; C
J. Exp. Med. 167, 1939-1944, 1988
A:Title: Cloning and characterization of a cDNA for murine macrophage inflammatory protei
A:Reference number: S04533; MUID:88258380; PMID:3290382
A:Accession: S04533
A:Molecule type: mRNA
A:Residues: 1-48, 'E', 50-90, 'T', 92 <DA2>
A:Cross-references: UNIPARC:UPI0000176749; EMBL:X12531
A:Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue 91
R:Davidellis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.; C
J. Exp. Med. 170, 2189, 1989
A:Reference number: A53885
A:Contents: extratun
A:Accession: A53885
A:Molecule type: mRNA
A:Residues: 1-92 <DAV>

A;Cross-references: UNIPARC:UPI0000020B06; EMBL:X12531; NID:953122; PIDN:CAA31047.1; PID: R; Brown, K.D.; Zurawski, S.M.; Moemann, T.R.; Zurawski, G.
 J; Immunol. 142, 679-687, 1989
 A;Title: A family of small inducible proteins secreted by leukocytes are members of a new class of various activation processes
 A;Reference number: A50552; MUID:69093958; PMID:2521353
 A;Accession: A50552
 A;Molecule type: mRNA
 A;Residues: 1-21, 'V', 23-61, 'A', 63-92

 A;Cross-references: UNIPARC:UPI000016D05B; GB:M23447; NID:G533240; PIDN:AAA40146.1; PID: R; Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mac U. Exp. Med. 168, 2251-2259, 1988
 A;Title: Resolution of the two components of macrophage inflammatory protein 1, and cloning
 A;Reference number: J10088; MUID:89067830; PMID:3058836
 A;Accession: PS0303
 A;Molecule type: mRNA
 A;Residues: 24-33, 'XX', 36-54 <SHE>
 A;Cross-references: UNIPARC:UPI000017674A
 R; Molpe, S.D.; Davatelis, G.; Sherry, B.; Beutler, B.; Heese, D.G.; Nguyen, H.T.; Moldaw U. Exp. Med. 167, 570-581, 1988
 A;Title: Macrophages secrete a novel heparin-binding protein with inflammatory and neutralizing activity
 A;Reference number: A27596; MUID:88154745; PMID:3279154
 A;Accession: A27596
 A;Molecule type: protein
 A;Residues: 24-33, 'XX', 36-42 <MOL>
 A;Cross-references: UNIPARC:UPI000017674B
 A;Note: 26-Met, 30-Pro, and 39-Thr were also found
 R; Widmer, U.; Yang, Z.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.
 J. Immunol. 146, 4031-4040, 1991
 A;Title: Genomic structure of murine macrophage inflammatory protein-1-alpha and conservation
 A;Reference number: 156104; MUID:91237116; PMID:2033269
 A;Accession: 156104
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-92 <RES>
 A;Cross-references: UNIPARC:UPI000020B06; GB:M73061; NID:G19694; PIDN:AAA39707.1; PID: C; Comment: This protein is a monokine.
 C;Genetics:
 A;Intons: 23/3; 26/1; 63/2
 C;Superfamily: macrophage inflammatory protein
 C;Keywords: heparin binding
 P;1-23/Domin: signal sequence #status predicted <SIG>
 P;24-92/Product: macrophage inflammatory protein #status experimental <MAT>
 Query Match 48.2%; Score 200.5; DB 2; Length 92;
 Best Local Similarity 48.6%; Pred. No. 1.8e-15; Indels 1; Gaps 1;
 Matches 34; Conservative 17; Mismatches 18; Indels 1; Gaps 1;
 Oy 5 SSSRGPHNPSCEFTYTKIPRORIMDYETNSQSKPGIVFTKRGHSVCTNPSPDKV 64
 Db 23 SARYGADTPFACCFSGR-QIPKRFADYFTSSLSQSPGVITLRNRQICADPKETW 81
 Oy 65 ODYIKMKEN 74
 Db 82 QSRITTELELN 91
 RESULT 7
 152322
 Macrophage inflammatory protein-1alpha - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 A;Accession: 152322
 R;Shi, M.W.; Godleski, J.J.; Paulauskis, J.D.
 Biochem. Biophys. Res. Commun. 211, 289-295, 1995
 A;Title: Molecular cloning and posttranscriptional regulation of macrophage inflammatory protein-1
 A;Reference number: 152322; MUID:95298037; PMID:7779098
 A;Accession: 152322
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-92 <RES>
 A;Cross-references: UNIPROT:P50229; UNIPARC:UPI00001362CA; EMBL:U22414; NID:G790632; PID: C; Superfamily: macrophage inflammatory protein

Query Match 46.0%; Score 191.5; DB 2; Length 92;
 Best Local Similarity 45.7%; Pred. No. 1.8e-14; Indels 1; Gaps 1;
 Matches 33; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
 Oy 5 SSSRGPHNPSCEFTYTKIPRORIMDYETNSQSKPGIVFTKRGHSVCTNPSPDKV 64
 Db 23 SARYGADTPFACCFSGR-QIPKRFADYFTSSLSQSPGVITLRNRQICADPKETW 81
 Oy 65 ODYIKMKEN 74
 Db 82 QSRITTELELN 91
 RESULT 8
 A28815
 monocyte chemoattractant cytokine RANTES precursor - human
 N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1989 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 A;Accession: A28815
 R;Schall, T.J.; Jongstere, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.; Krut J. Immunol. 141, 1018-1025, 1988
 A;Title: A human T cell-specific molecule is a member of a new gene family.
 A;Reference number: A28815; MUID:88285659; PMID:2456327
 A;Accession: A28815
 A;Molecule type: mRNA
 A;Residues: 1-91 <SCH>
 A;Cross-references: UNIPROT:P13501; UNIPARC:UPI000004A187; GB:M21121
 C;Comment: The acronym RANTES reflects the description "Regulated upon Activation, Normal" and "T-cell Attractant Secreted".
 C;Genetics:
 A;Gene: GDB:SCYAS; D17S136E
 A;Cross-references: GDB:120749; OMIM:187011
 A;Map position: 17q11.2-17q12
 C;Superfamily: macrophage inflammatory protein
 C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell
 P;1-23/Domin: signal sequence #status predicted <SIG>
 P;24-91/Product: T-cell protein RANTES #status predicted <MAT>
 Query Match 41.3%; Score 172; DB 1; Length 91;
 Best Local Similarity 39.1%; Pred. No. 2.8e-12; Indels 2; Gaps 1;
 Matches 27; Conservative 15; Mismatches 25; Indels 2; Gaps 1;
 Oy 6 SSSRGPHNPSCEFTYTKIPRORIMDYETNSQSKPGIVFTKRGHSVCTNPSPDKV 63
 Db 21 ASASPYGSDTTPCCFVIANPLPRAHKEYFTSGKCSNDAVVFVTRKNQVCANPEKVV 80
 Oy 64 VODYIKDMK 72
 Db 81 VREYINSL 89
 RESULT 9
 A46539
 monocyte chemoattractant cytokine RANTES precursor - mouse
 N;Alternate names: Murantes
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 A;Accession: 148875; A46539; T48654; I56970
 R;Danbolt, T.W.; Lallier, E.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.
 J. Immunol. 152, 1182-1189, 1994
 A;Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene
 A;Reference number: 148875; MUID:94132613; PMID:7507961
 A;Accession: 148875
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-91 <DNA>
 A;Cross-references: UNIPROT:P30882; UNIPARC:UPI000002028C; EMBL:U02298; NID:9460090; PID: R; Schall, T.J.; Simpson, N.J.; Mak, J.Y.
 Eur. J. Immunol. 22, 1477-1481, 1992
 A;Title: Molecular cloning and expression of the murine RANTES cytokine: structural and functional analysis
 A;Reference number: A46539; MUID:92289805; PMID:1376260
 A;Accession: A46539

A: Molecule type: mRNA
 A:Residues: 1-18, 'A', 20-91 <SCH>
 A:Cross-references: UNIPARC:UPI0000015811; GB:S37648; NID:9250207; PIDN:AA22330.1; PID:
 A:Experimental source: macrophage cell line PUS-1.8
 A:Note: Sequence extracted from NCBI backbone (NCBIN:106768, NCBI:P:106770)
 R:Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.
 Mol. Cell. Biol. 14, 2914-2925, 1994
 A:Title: Definition of a 110poyascharide-responsive element in the 5'-flanking region
 A:Reference number: 148654; MUID:94217689; PMID:7513046
 A:Accession: 148654
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-91 <SH1>
 A:Cross-references: UNIPARC:UPI000000028C; EMBL:X70675; NID:9475205; PIDN:CA50011.1; PI:
 R:Neelson, E.G.; Krensky, A.
 Kidney Int. 41, 220-225, 1992
 A:Title: Isolation and characterization of cDNA from renal tubular epithelium encoding m
 A:Reference number: 156970; MUID:92277990; PMID:1375672
 A:Accession: 156970
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-40, 'E', 42-91 <NEI>
 A:Cross-references: UNIPARC:UPI000016380F; GB:M77747; NID:9200649; PIDN:AAA40029.1; PID:
 C:Comment: This chemoattractant for monocytes but not neutrophils is an immediate-early
 C:Genetics: 26/1; 63/2
 A:Introns: 26/1; 63/2
 C:Superfamily: macrophage inflammatory protein
 C:Keywords: chemotaxis; cytokine; immediate-early protein; inflammation
 F:1-23/Pomatin: signal sequence #status predicted <SIG>
 F:24-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MNT>
 Query Match 40.1%; Score 167; DB 1; Length 91;
 Best Local Similarity 44.3%; Pred. No. 1e-11;
 Matches 27; Conservative 12; Mismatches 20; Indels 2; Gaps 1;
 QY 10 PY--HPSECCFTYTKIPROIMDYETNSQSGKPGVFTTKGHSVCTNPSDKWVDYTKD 67
 DB 25 PYGSDTTPCCFAYLALPRAHVKEFYTSKCSNLAVFTRRURQVCANPEKKWQERY 84
 QY 68 I 68
 DB 85 I 85
 RESULT 10
 JB0177
 lymphocyte and monocyte chemoattractant CC chemokine - human
 C:Species: Homo sapiens (man)
 C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
 C:Accession: JB0177
 A:Residues: 1-120 <YOU>
 A:Cross-references: UNIPARC:UPI000017C296
 Query Match 39.3%; Score 163.5; DB 2; Length 120;
 Best Local Similarity 50.0%; Pred. No. 3.3e-11;
 Matches 29; Conservative 8; Mismatches 20; Indels 1; Gaps 1;
 QY 13 PSECCFTYTKIPROIMDYETNSQSGKPGVFTTKGHSVCTNPSDKWVDYTKD 70
 DB 34 PSTCCKLYTE-KVLEKRLVGVGKALNCHLPIIIFTKKREVCITPNPNDMDQGEYIKD 90
 RESULT 11
 C60407
 monocyte adherence-induced protein 5 beta - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 31-Dec-2004

C:Accession: C60407
 R:Sporn, S.A.; Eierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haskell,
 J. Immunol. 144, 4434-4441, 1990
 A:Title: Monocyte adherence results in selective induction of novel genes sharing homolog
 A:Reference number: A60407; MUID:90257367; PMID:2341726
 A:Accession: C60407
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-50 <SPO>
 A:Cross-references: UNIPROT:Q8NFM4; UNIPARC:UPI0000176747
 Query Match 39.2%; Score 163; DB 2; Length 50;
 Best Local Similarity 52.0%; Pred. No. 1.6e-11;
 Matches 26; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
 QY 25 IPROIMDYETNSQSGKPGVFTTKGHSVCTNPSDKWVDYTKDKEN 74
 DB 1 VPRNFVVDYETSSICSQPAVFPQKSKQVCADPSESWMQEVYVDLELN 50
 RESULT 12
 149555
 gene C10 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 149555
 R:Orlowski, A.; Berger, M.S.; Pyzrowsky, M.B.
 Cell Regul. 2, 403-412, 1991
 A:Title: Novel expression pattern of a new member of the MIP-1 family of cytokine-like ge
 A:Reference number: 149555; MUID:91370083; PMID:1832565
 A:Accession: 149555
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-116 <RES>
 A:Cross-references: UNIPROT:P27784; UNIPARC:UPI000000028D; GB:M58004; NID:9192243; PIDN:
 C:Genetics: 4
 A:Gene: C10
 C:Superfamily: macrophage inflammatory protein
 Query Match 37.9%; Score 157.5; DB 2; Length 116;
 Best Local Similarity 46.7%; Pred. No. 1.5e-10;
 Matches 28; Conservative 15; Mismatches 16; Indels 1; Gaps 1;
 QY 14 SECCFTYTKIPROIMDYETNSQSGKPGVFTTKGHSVCTNPSDKWVDYTKDKKE 73
 DB 48 SDCCFSYAT-QIPCKRFYFPTSGGCTKPGIIFISKGTQVCADPDRVRCLSTLKQ 106
 RESULT 13
 A30209
 PDGF-inducible JE glycoprotein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A30209; A44771; A30861
 R:Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
 A:Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor
 A:Reference number: A30209; MUID:88234501; PMID:3287374
 A:Accession: A30209
 A:Molecule type: DNA
 A:Residues: 1-148 <ROU>
 A:Cross-references: UNIPROT:P10148; UNIPARC:UPI0000020A69; GB:M19681; NID:9193486; PIDN:
 R:Kawahara, R.S.; Deuel, T.F.
 J. Biol. Chem. 264, 679-682, 1989
 A:Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma
 A:Reference number: A44771; MUID:89093129; PMID:2910858
 A:Accession: A44771
 A:Molecule type: DNA; mRNA
 A:Residues: 1-148 <KA2>
 A:Cross-references: UNIPARC:UPI0000020A69; GB:J04467; NID:9193488; PIDN:AAA37685.1; PID:
 C:Genetics: 4
 A:Gene: JE
 A:Introns: 26/1; 65/2

C/Superfamily: macrophage inflammatory protein
 C/Keywords: cytokine; glycoprotein
 F/126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.2%; Score 150.5; DB 1; Length 148;
 Best Local Similarity 41.3%; Pred. No. 1.2e-09;
 Matches 26; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 13 PSECCFTYTYTKIPROIMDYE-TNSQSKPGIVFTKRGHSVCTNPSDKWQDYIKDM 71
 DB 31 PLTCCYSFTGKMIPLMSRLSEYKRTSSRCPEAVVFTKLRKREVCADPKKEMVQTYIKNL 90

QY 72 KEN 74
 DB 91 DRN 93

RESULT 14
 JCS295
 monocytic chemotactic protein-2 precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
 C/Accession: JCS295
 R/Van Collille, B.; Froyen, G.; Nomiyama, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van De Biochem. Biophys. Res. Commun. 231, 726-730, 1997
 A/Title: Human monocytic chemotactic protein-2: cDNA cloning and regulated expression of A/Reference number: JCS295; MUID:97224420; PMID:9070881
 A/Accession: JCS295
 A/Molecule type: mRNA
 A/Residues: 1-99 <VAN>
 A/Cross-references: UNIPROT:P80075; UNIPARC:UPI0000030FC6; GB:Y10802; NID:G1924937; PIDN A/Experimental source: bone marrow
 C/Comment: This protein belongs to the beta-chemokine family which is one of the major H its and in tumor biology, and contribute to the trafficking and recruitment of the respo C/Genetics:
 A/Gene: MCP-2
 C/Superfamily: macrophage inflammatory protein
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-99/Product: monocytic chemotactic protein-2 #status predicted <MAT>

Query Match 35.0%; Score 145.5; DB 2; Length 99;
 Best Local Similarity 41.9%; Pred. No. 2.8e-09;
 Matches 26; Conservative 11; Mismatches 24; Indels 1; Gaps 1;

QY 13 PSECCFTYTYTKIPROIMDYE-TNSQSKPGIVFTKRGHSVCTNPSDKWQDYIKDM 71
 DB 31 PLTCCYFVNRKTIQRLSEYTRITINIQCPKAVVFTKRGKVCADPKKEMVQDYIKNL 90

QY 72 KEN 73
 DB 91 DQ 92

RESULT 15
 S07723
 Immediate-early serum-responsive protein JE precursor - rat
 N/Alternate names: monocytic chemottractant protein-1
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: S07723; JN0128
 R/Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
 Nucleic Acids Res. 18, 23-34, 1990
 A/Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential A/Reference number: S07723; MUID:90174947; PMID:2106664
 A/Accession: S07723
 A/Molecule type: DNA
 A/Residues: 1-148 <TIM>
 A/Cross-references: UNIPROT:P14844; UNIPARC:UPI0000000187; EMBL:X17053; NID:G55530; PIDN R/Yoshimura, T.; Takeya, M.; Takahashi, K.
 Biochem. Biophys. Res. Commun. 174, 504-509, 1991
 A/Title: Molecular cloning of rat monocytic chemottractant protein-1 (MCP-1) and its exp A/Reference number: JN0128; MUID:91128376; PMID:1704226
 A/Accession: JN0128

A/Molecule type: mRNA
 A/Residues: 1-148 <YOS>
 A/Cross-references: UNIPARC:UPI0000000187; GB:M57441; NID:G205333; PIDN:AAA63496.1; PID:5
 A/Experimental source: spleen cells
 A/Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue 63
 C/Genetics:
 A/Insertions: 26/1; 65/2
 C/Superfamily: macrophage inflammatory protein
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>

Query Match 35.0%; Score 145.5; DB 1; Length 148;
 Best Local Similarity 38.1%; Pred. No. 4.2e-09;
 Matches 24; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 13 PSECCFTYTYTKIPROIMDYE-TNSQSKPGIVFTKRGHSVCTNPSDKWQDYIKDM 71
 DB 31 PLTCCYSFTGKMIPLMSRLSEYKRTSSRCPEAVVFTKLRKREVCADPKKEMVQTYIKNL 90

QY 72 KEN 74
 DB 91 DQ 93

Search completed: January 10, 2006, 23:00:09
 Job time : 39 secs